STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/048,116A_
Source: _1FwI16_
Date Processed by STIC: _12/29/05_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street. Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: *10/048,116A* |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ___ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ___ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length — Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 [✓] PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) *2,4,6,8*. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ___ Skipped Sequences (OLD RULES) — Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ___ Skipped Sequences (NEW RULES) — Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ___ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220> — Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n/Xaa — "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003
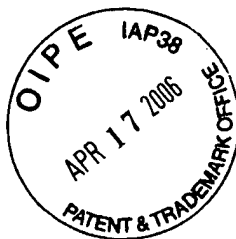
IPW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/048,116A

DATE: 12/29/2005
TIME: 12:20:15

Input Set : A:\seq list.txt
Output Set: N:\CRF4\12292005\J048116A.raw

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 3 <110> APPLICANT: CNRS
 5 <120> TITLE OF INVENTION: RECOMBINANT PROTEINS AND MOLECULAR COMPLEXES DERIVED
 6       FROM THESE PROTEINS, ANALOGOUS TO MOLECULES INVOLVED IN
 7       IMMUNE RESPONSES
 9 <130> FILE REFERENCE: 1721-47
11 <140> CURRENT APPLICATION NUMBER: 10/048,116A
12 <141> CURRENT FILING DATE: 2002-02-27
14 <150> PRIOR APPLICATION NUMBER: PCT/FR00/02193
15 <151> PRIOR FILING DATE: 2000-07-28
17 <150> PRIOR APPLICATION NUMBER: FR99/09862
18 <151> PRIOR FILING DATE: 1999-07-29
20 <160> NUMBER OF SEQ ID NOS: 8
22 <170> SOFTWARE: PatentIn Ver. 2.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1517
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Description of Artificial Sequence: construct
31       coding IAalpha(d)/Fc
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (18)..(1502)
37 <400> SEQUENCE: 1
38 aaagggggga attcagg atg ccg tgc agc aga gct ctg att ctg ggg gtc     50
39                     Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val
40                      1               5                  10
42 ctc gcc ctg aac acc atg ctc agc ctc tgc gga ggt gaa gac gac att    98
43 Leu Ala Leu Asn Thr Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile
44             15                  20                  25
46 gag gcc gac cac gta ggc ttc tat ggt aca act gtt tat cag tct cct   146
47 Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro
48         30                  35                  40
50 gga gac att ggc cag tac aca cat gaa ttt gat ggt gat gag ttg ttc   194
51 Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe
52         45                  50                  55
54 tat gtg gac ttg gat aag aag aaa act gtc tgg agg ctt cct gag ttt   242
55 Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe
56  60                  65                  70                  75
58 ggc caa ttg ata ctc ttt gag ccc caa ggt gga ctg caa aac ata gct   290
59 Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala
60                  80                  85                  90
62 gca gaa aaa cac aac ttg gga atc ttg act aag agg tca aat ttc acc   338
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63 Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr
64          95                  100                 105
66 cca gct acc aat gag gct cct caa gcg act gtg ttc ccc aag tcc cct    386
67 Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro
68          110                 115                 120
70 gtg ctg ctg ggt cag ccc aac acc ctt atc tgc ttt gtg gac aac atc    434
71 Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile
72     125                 130                 135
74 ttc cca cct gtg atc aac atc aca tgg ctc aga aat agc aag tca gtc    482
75 Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val
76 140                 145                 150                 155
78 aca gac ggc gtt tat gag acc agc ttc ctc gtc aac cgt gac cat tcc    530
79 Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser
80                      160                 165                 170
82 ttc cac aag ctg tct tat ctc acc ttc atc cct tct gat gat gac att    578
83 Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile
84          175                 180                 185
86 tat gac tgc aag gtg gag cac tgg ggc ctg gag gag ccg gtt ctg aaa    626
87 Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys
88          190                 195                 200
90 cac tgg gaa cct gag att cca gcc ccc atg tca gag ctg aca gaa act    674
91 His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr
92     205                 210                 215
94 gga ggt gga gga tcc act aca gct cca tca gct cag ctc gaa aaa gag    722
95 Gly Gly Gly Gly Ser Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu
96 220                 225                 230                 235
98 ctc cag gcc ctg gag aag gaa aat gca cag ctg gaa tgg gag ttg caa    770
99 Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln
100                 240                 245                 250
102 gca ctg gaa aag gaa ctg gct cag gca gca tct gag ccc aga ggg ccc   818
103 Ala Leu Glu Lys Glu Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro
104             255                 260                 265
106 aca atc aag ccc tgt cct cca tgc aaa tgc cca gca cct aac ctc ttg   866
107 Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu
108             270                 275                 280
110 ggt gga cca tcc gtc ttc atc ttc cct cca aag atc aag gat gta ctc   914
111 Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu
112     285                 290                 295
114 atg atc tcc ctg agc ccc ata gtc aca tgt gtg gtg gtg gat gtg agc   962
115 Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser
116 300                 305                 310                 315
118 gag gat gac cca gat gtc cag atc agc tgg ttt gtg aac aac gtg gaa   1010
119 Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu
120                 320                 325                 330
122 gta cac aca gct cag aca caa acc cat aga gag gat tac aac agt act   1058
123 Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr
124             335                 340                 345
126 ctc cgg gtg gtc agt gcc ctc ccc atc cag cac cag gac tgg atg agt   1106
127 Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser
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RAW SEQUENCE LISTING   DATE: 12/29/2005
PATENT APPLICATION: US/10/048,116A   TIME: 12:20:15

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Output Set: N:\CRF4\12292005\J048116A.raw

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128         350                355                360
130 ggc aag gag ttc aaa tgc aag gtc aac aac aaa gac ctc cca gcg ccc    1154
131 Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro
132         365                370                375
134 atc gag aga acc atc tca aaa ccc aaa ggg tca gta aga gct cca cag    1202
135 Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln
136 380                385                390                395
138 gta tat gtc ttg cct cca cca gaa gaa gag atg act aag aaa cag gtc    1250
139 Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val
140                400                405                410
142 act ctg acc tgc atg gtc aca gac ttc atg cct gaa gac att tac gtg    1298
143 Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val
144         415                420                425
146 gag tgg acc aac aac ggg aaa aca gag cta aac tac aag aac act gaa    1346
147 Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu
148         430                435                440
150 cca gtc ctg gac tct gat ggt tct tac ttc atg tac agc aag ctg aga    1394
151 Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg
152         445                450                455
154 gtg gaa aag aag aac tgg gtg gaa aga aat agc tac tcc tgt tca gtg    1442
155 Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val
156 460                465                470                475
158 gtc cac gag ggt ctg cac aat cac cac acg act aag agc ttc tcc cgg    1490
159 Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg
160                480                485                490
162 act ccg ggt aaa tgatgactcg acctg                                   1517
163 Thr Pro Gly Lys
164                495
167 <210> SEQ ID NO: 2
168 <211> LENGTH: 495
169 <212> TYPE: PRT
170 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
172 <223> OTHER INFORMATION: see item 6 on Error Summary Sheet
172 <400> 2                                          (same
173 Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr    error in
174 1                  5                  10                 15         seqs. 4, 6, 8
176 Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val
177         20                 25                 30
179 Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln
180         35                 40                 45
182 Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp
183         50                 55                 60
185 Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu
186 65                 70                 75                 80
188 Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn
189         85                 90                 95
191 Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu
192         100                105                110
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W--> 172 <223> OTHER INFORMATION:
W--> 172 <400> 2

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194 Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln
195         115             120             125
197 Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile
198     130             135             140
200 Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr
201 145             150             155             160
203 Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser
204             165             170             175
206 Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val
207         180             185             190
209 Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu
210         195             200             205
212 Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Gly Gly Gly Gly Ser
213     210             215             220
215 Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu Leu Gln Ala Leu Glu
216 225             230             235             240
218 Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu
219             245             250             255
221 Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys
222         260             265             270
224 Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val
225         275             280             285
227 Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser
228     290             295             300
230 Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp
231 305             310             315             320
233 Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln
234             325             330             335
236 Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser
237             340             345             350
239 Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys
240         355             360             365
242 Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile
243     370             375             380
245 Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
246 385             390             395             400
248 Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
249             405             410             415
251 Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
252         420             425             430
254 Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
255         435             440             445
257 Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
258     450             455             460
260 Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
261 465             470             475             480
263 His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
264             485             490             495
267 <210> SEQ ID NO: 3
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RAW SEQUENCE LISTING   DATE: 12/29/2005
PATENT APPLICATION: US/10/048,116A   TIME: 12:20:15

Input Set : **A:\seq list.txt**
Output Set: **N:\CRF4\12292005\J048116A.raw**

268 <211> LENGTH: 1485
269 <212> TYPE: DNA
270 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:
273 <223> OTHER INFORMATION: Description of Artificial Sequence:coding region
274   of SEQ ID NO:1
276 <220> FEATURE:
277 <221> NAME/KEY: CDS
278 <222> LOCATION: (1)..(1485)
280 <400> SEQUENCE: 3
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282 Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr
283 1   5   10   15
285 atg ctc agc ctc tgc gga ggt gaa gac gac att gag gcc gac cac gta   96
286 Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val
287   20   25   30
289 ggc ttc tat ggt aca act gtt tat cag tct cct gga gac att ggc cag   144
290 Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln
291   35   40   45
293 tac aca cat gaa ttt gat ggt gat gag ttg ttc tat gtg gac ttg gat   192
294 Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp
295   50   55   60
297 aag aag aaa act gtc tgg agg ctt cct gag ttt ggc caa ttg ata ctc   240
298 Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu
299 65   70   75   80
301 ttt gag ccc caa ggt gga ctg caa aac ata gct gca gaa aaa cac aac   288
302 Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn
303   85   90   95
305 ttg gga atc ttg act aag agg tca aat ttc acc cca gct acc aat gag   336
306 Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu
307   100   105   110
309 gct cct caa gcg act gtg ttc ccc aag tcc cct gtg ctg ctg ggt cag   384
310 Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln
311   115   120   125
313 ccc aac acc ctt atc tgc ttt gtg gac aac atc ttc cca cct gtg atc   432
314 Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile
315   130   135   140
317 aac atc aca tgg ctc aga aat agc aag tca gtc aca gac ggc gtt tat   480
318 Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr
319 145   150   155   160
321 gag acc agc ttc ctc gtc aac cgt gac cat tcc ttc cac aag ctg tct   528
322 Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser
323   165   170   175
325 tat ctc acc ttc atc cct tct gat gat gac att tat gac tgc aag gtg   576
326 Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val
327   180   185   190
329 gag cac tgg ggc ctg gag gag ccg gtt ctg aaa cac tgg gaa cct gag   624
330 Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu
331   195   200   205

Input Set : **A:\seq list.txt**
Output Set: **N:\CRF4\12292005\J048116A.raw**

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ORGANISM:Artificial Sequence
L:172 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
ORGANISM:Artificial Sequence
L:172 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:172
L:411 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:4, <213>
ORGANISM:Artificial Sequence
L:411 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
ORGANISM:Artificial Sequence
L:411 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:411
L:606 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:606 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:606 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:606
L:768 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:768 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:768 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:768